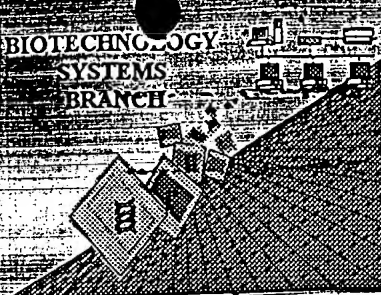


**RAW SEQUENCE LISTING
ERROR REPORT**

L. Gansheroff



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/236,995A
Source: 1638
Date Processed by STIC: 11/1/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

SERIAL NUMBER: **09/236,996A**

ERROR DETECTED SUGGESTED CORRECTION

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ **Use of <213> Organism (NEW RULES)** Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ **Use of <220> Feature (NEW RULES)** Sequence(s) _____ are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

O:Zagham

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/236,995A

DATE: 11/01/2000
TIME: 13:18:34

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Output Set : N:\CRF3\11012000\I236995A.raw

Does Not Comply
Corrected Diskette Needed

see 2-7
PP-6-7

3 <110> APPLICANT: Mahajan, Pramod B.
4 Zuo, Zhuang
6 <120> TITLE OF INVENTION: Poly ADP-Ribose Polymerase Gene and Its Uses
8 <130> FILE REFERENCE: 5718-34, 035718-174234
10 <140> CURRENT APPLICATION NUMBER: 09/236,995A
11 <141> CURRENT FILING DATE: 1999-01-26
13 <150> PRIOR APPLICATION NUMBER: 60/072,785
14 <151> PRIOR FILING DATE: 1998-01-27
16 <160> NUMBER OF SEQ ID NOS: 5
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2949
22 <212> TYPE: DNA
23 <213> ORGANISM: Zea mays
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27 <222> LOCATION: (1)..(2949)
29 <220> FEATURE:
30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: (1)..()
32 <223> OTHER INFORMATION: nA, T, C, or G
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44 cag gcc tgg tgc aag tca tgc cga tcc ctt atc gcc aag gac cag ctc 96
45 Arg Ala Ser Cys Lys Ser Cys Arg Ser Pro Ile Ala Lys Asp Gln Leu
46 20 25 30
48 cgt ctt gcc aag atg gtl cag cag tca cag ttc gac gcc ttc atg ccg 144
49 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
50 35 40 45
52 atg tgg aac cat gcc agg tgc atc ttc agc aag aag aac cag ata aag 192
53 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
54 50 55 60
56 tcc gtt gac gat gtl gaa gga ata gat gca ctt aga tgg gat gat gaa 240
57 Ser Val Asp Asp Val Gln Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
58 65 70 75 80
60 gag aag ata cga aac tac gtl ggg ggt gcc tca gct ggt aca agt tct 288
61 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
62 85 90 95
64 aca gct gct cct cct gag aag tat aca att gaa att gct cca tct gcc 336
65 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
66 100 105 110

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/236,995A

DATE: 11/01/2000

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70 115 120 125
72 cgt ctt tca gct aag ctt gag agt gaa ggt ccc aag ggt ata cca tgg 432
73 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
74 130 135 140
76 tat cat gcc aac tgt ttc ttt gag gta tcc ccg tct gca act gtt gag 480
77 Tyr His Ala Asn Cys Phe Glu Val Ser Pro Ser Ala Thr Val Glu
78 145 150 155 160
80 aag ttc tca ggc tgg gat act ttg tcc gat gag gat aag aga acc atg 528
81 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
82 165 170 175
84 ctc gat ctt gtt aaa aaa gat gtt ggc aac aat gaa caa aat aag ggt 576
85 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Gln Asn Lys Gly
86 180 185 190
88 tcc aag cgc aag aau agt gaa aat gat att gat agc tac aaa tcc gcc 624
89 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
90 195 200 205
92 aag tta gat gaa agt aca tct gaa qgt aca gtc cga aac aaa ggg caa 672
93 Arg Leu Asp Glu Ser Thr Ser Glu Gly Thr Val Arg Asn Lys Gly Gln
94 210 215 220
96 ctt gta gac cca cgt qgt tcc aat act agt tca gct gat atc caa cta 720
97 Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
98 225 230 235 240
100 aag ctt aag gaa caa aat gac aca ctt tgg aag tta aag gat qga ctt 768
101 Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
102 245 250 255
104 aag act cat gta tcc gct gct gaa tta agg gat atg ctt gag gct aat 816
105 Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
106 260 265 270
108 ggg cag gat aca tca gga cca gaa aag cac cta ttg gat cgc tgt cgc 864
109 Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
110 275 280 285
112 gat gga atg cta tat gga ggc ctg qgt cct tgc cca gtc tgt gct aat 912
113 Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
114 290 295 300
116 ggc atg tac tat tat aat ggt cag tac caa tgc agt ggt aat gtc tca 960
117 Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
118 305 310 315 320
120 aag tgg tcc aag tgt aca tcc tct gcc aca gaa cct gtc cgc gtt aag 1008
121 Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
122 325 330 335
124 aag aag tgg caa att cca cat gga aca aag aat gat tac ctt atg aag 1056
125 Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
126 340 345 350
128 tgg ttc aaa tct caa aag gtt aag aca gag agt gtt ctt cca cca 1104
129 Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
130 355 360 365
132 atg tca cct gag aca tct gga agt aca gca act cag aga aca tca ttg 1152

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RAW SEQUENCE LISTING

DATE: 11/01/2000

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TIME: 13:18:34

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138 385 390 395 400
140 tca aaa gaa gca gca aat gag tgg att gag aag ctc aaa ctt gct ggt 1248
141 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly
142 405 410 415
144 gcc aac ttc tat gcc agg gtt gtc aaa gat att gat tgt tta att gca 1296
145 Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
146 420 425 430
148 tat gat gag ctg gac aat gaa aat gct gaa gtc agg aaa gca agg agg 1344
149 Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
150 435 440 445
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153 Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys
154 450 455 460
156 aga aca aaa tgc tgc cat ttg att tgt ata aac tgg aat gcc tta gag 1440
157 Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
158 465 470 475 480
160 tcc tca aaa gcc mgt act gtc act gtt aaa gtt aag gcc cga aqt gct 1488
W--> 161 Ser Ser Lys Gly Xaa Thr Val Lys Val Lys Gly Arg Ser Ala
162 485 490 495
164 tat tca tta aat act cgg gtt tgc aag aat act gct cac att cct tra 1536
W--> 165 Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
166 500 505 510
168 gra tgg gaa aag cat ata caa tgc amc ctt aaa cat gtt ctg acc tgn 1584
W--> 169 Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
170 515 520 525
172 cac nag gtg tgy aca ggc tac tat gta ctc cag atc att gaa cag gat 1632
W--> 173 His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp
174 530 535 540
176 gat qgg tct aag tgc tac gta ttt cgt aag tgg gga cgg gtt qgg aqt 1680
177 Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
178 545 550 555 560
180 gga aaa att qga qgg cca aaa ctg gag gag atg tca aaa act gag gca 1728
181 Gln Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
182 565 570 575
184 atc aag gaa ttc aaa aga tta ttt ctt gag aag act gga aac tca tgg 1776
185 Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
186 580 585 590
188 gaa gct tgg gaa tgt aaa acc aat ttt cgg aag cag cct qgg aga ttt 1824
189 Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
190 595 600 605
192 tcc cca ctt gat gtt gat tat ggt gtt aag aaa gca cca aaa cgg aat 1872
193 Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
194 610 615 620
196 gat atc aqt gaa atg aaa aqt tct ctt gct cct caa ttg cta gaa ctc 1920
197 Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/236,995A

DATE: 11/01/2000

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204	ttt gaa awt aat atg tca gaa atg cct ctt ggg aag cta agc mag gra	2016			
W--> 205	Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa				
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W--> 212	gaa gga cac cgc tna tca agc act ggc ttg ttr gag aaa gct naa ttg	2112			
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216	ttg ttg sga gcm ats syt ttt tca ctc tta tcc ctt cta ttc atc ctc	2160			
W--> 217	Leu Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu				
218	705	710	715	720	
220	ata tta tac ggg atg agg atg att tca tat tca bag gcg aaa atg ctt	2208			
221	Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu				
222	725	730	735		
224	gaa gct ctg caa gat att gaa att gct tca aag ata gtt agc ttc gat	2256			
225	Glu Ala Leu Glu Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp				
226	740	745	750		
228	agc gac agt gat gaa tct ctt gat gat aac tat atg aaa ctt cgc tgn	2304			
229	Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys				
230	755	760	765		
232	gac atc acc ccg ctg gct cac gat agt gaa aat tac aag tta att gag	2352			
233	Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Phe Lys Leu Ile Glu				
234	770	775	780		
236	caq tat ctc ctc aac aca cat gct cct act aac aag gac tgg tca ctg	2400			
237	Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu				
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240	gaa ctg qag gaa gtt ttt tca ctt gat cga gat aag gaa ctt aat aag	2448			
241	Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys				
242	805	810	815		
244	tac tca aga tat aca aat aat ctg cat aac aag atg cta tta tgg cac	2496			
245	Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His				
246	820	825	830		
248	ggt tca agg ttg acg aat ttt gtg gga att ctt agt aag ggg cta aag	2544			
249	Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Glu Gly Leu Arg				
250	835	840	845		
252	att aca cct cct gag gca cct gtt act gac tat atg ttc aac aat gac	2592			
253	Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly				
254	850	855	860		
256	ctc tac ttt gca gat cta gta agc aag aac aca tac tgt tat gta	2640			
257	Leu Tyr Phe Ala Asp Leu Val Ser Lys Ser Ala Glu Tyr Cys Tyr Val				
258	865	870	875	880	
260	gat agg aat aat cct gta ggt ttg atg ctt ctt tct gag gtt gct tta	2688			
261	Asp Arg Asn Asn Pro Val Gly Leu Met Leu Leu Ser Glu Val Ala Leu				
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RAW SEQUENCE LISTING

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266 900 905 910
268 aga ggg aag cat tcg acc aag gga tta ggc aaa acc gtg cca ctg gag 2784
269 Arg Gly Lys His Ser Thr Lys Gly Leu Gly Lys Thr Val Pro Leu Glu
270 915 920 925
272 tca gag ttt gtg aag tgg agg gat gat gtc gta gtt ccc tgc ggc aag 2832
273 Ser Glu Phe Val Lys Trp Arg Asp Asp Val Val Val Pro Cys Gly Lys
274 930 935 940
276 ccg gtg cca tca tca att agg agc tct gaa ctc atg tac aat gag tac 2880
277 Pro Val Pro Ser Ser Ile Arg Ser Ser Glu Leu Met Tyr Asn Glu Tyr
278 945 950 955
280 atc gtc tac aac aca tcc cag gtg aag atg cag ttc ttg ctg aag gtg 2928
281 Ile Val Tyr Asn Thr Ser Glu Val Lys Met Glu Phe Leu Leu Lys Val
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298 20 25 30
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300 35 40 45
301 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Glu Ile Lys
302 50 55 60
303 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Glu
304 65 70 75 80
305 Glu Lys Ile Arg Asn Phe Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
306 85 90 95
307 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
308 100 105 110
309 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
310 115 120 125
311 Arg Leu Ser Ala Lys Leu Glu Ser Glu Gly Pro Lys Gly Ile Pro Trp
312 130 135 140
313 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
314 145 150 155 160
315 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
316 165 170 175
317 Leu Asp Leu Val Lys Lys Asp Val Gly Asn Asn Glu Glu Asn Lys Gly
318 180 185 190
319 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
320 195 200 205

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see pp 6-7

<210> 2
 <211> 982
 <212> PRT
 <213> Zea mays

see next page

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 Arg Leu Gly Lys Met Val Gln Ala Ser Gln Phe Asp Gly Phe Met Pro
 35 40 45
 Met Trp Asn His Ala Arg Cys Ile Phe Ser Lys Lys Asn Gln Ile Lys
 50 55 60
 Ser Val Asp Asp Val Glu Gly Ile Asp Ala Leu Arg Trp Asp Asp Gln
 65 70 75 80
 Glu Lys Ile Arg Asn Tyr Val Gly Ser Ala Ser Ala Gly Thr Ser Ser
 85 90 95
 Thr Ala Ala Pro Pro Glu Lys Cys Thr Ile Glu Ile Ala Pro Ser Ala
 100 105 110
 Arg Thr Ser Cys Arg Arg Cys Ser Glu Lys Ile Thr Lys Gly Ser Val
 115 120 125
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 130 135 140
 Tyr His Ala Asn Cys Phe Phe Glu Val Ser Pro Ser Ala Thr Val Glu
 145 150 155 160
 Lys Phe Ser Gly Trp Asp Thr Leu Ser Asp Glu Asp Lys Arg Thr Met
 165 170 175
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 180 185 190
 Ser Lys Arg Lys Lys Ser Glu Asn Asp Ile Asp Ser Tyr Lys Ser Ala
 195 200 205
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 210 215 220
 Leu Val Asp Pro Arg Gly Ser Asn Thr Ser Ser Ala Asp Ile Gln Leu
 225 230 235 240
 Lys Leu Lys Glu Gln Ser Asp Thr Leu Trp Lys Leu Lys Asp Gly Leu
 245 250 255
 Lys Thr His Val Ser Ala Ala Glu Leu Arg Asp Met Leu Glu Ala Asn
 260 265 270
 Gly Gln Asp Thr Ser Gly Pro Glu Arg His Leu Leu Asp Arg Cys Ala
 275 280 285
 Asp Gly Met Leu Phe Gly Ala Leu Gly Pro Cys Pro Val Cys Ala Asn
 290 295 300
 Gly Met Tyr Tyr Tyr Asn Gly Gln Tyr Gln Cys Ser Gly Asn Val Ser
 305 310 315 320
 Glu Trp Ser Lys Cys Thr Tyr Ser Ala Thr Glu Pro Val Arg Val Lys
 325 330 335
 Lys Lys Trp Gln Ile Pro His Gly Thr Lys Asn Asp Tyr Leu Met Lys
 340 345 350
 Trp Phe Lys Ser Gln Lys Val Lys Lys Pro Glu Arg Val Leu Pro Pro
 355 360 365
 Met Ser Pro Glu Lys Ser Gly Ser Lys Ala Thr Gln Arg Thr Ser Leu
 370 375 380
 Leu Ser Ser Lys Gly Leu Asp Lys Leu Arg Phe Ser Val Val Gly Gln
 385 390 395 400
 Ser Lys Glu Ala Ala Asn Glu Trp Ile Glu Lys Leu Lys Leu Ala Gly

09/23/99

9

405 410 415
Ala Asn Phe Tyr Ala Arg Val Val Lys Asp Ile Asp Cys Leu Ile Ala
420 425 430
Cys Gly Glu Leu Asp Asn Glu Asn Ala Glu Val Arg Lys Ala Arg Arg
435 440 445
Leu Lys Ile Pro Ile Val Arg Glu Gly Tyr Ile Gly Glu Cys Val Lys,
450 455 460
Arg Thr Lys Cys Cys His Leu Ile Cys Ile Asn Trp Asn Ala Leu Glu
465 470 475
Ser Ser Lys Gly Xaa Thr Val Thr Val Lys Val Lys Gly Arg Ser Ala
485 490 495
Cys Ser Xaa Ser Pro Xaa Val Cys Lys Asn Thr Ala His Ile Pro Xaa
500 505 510
Xaa Trp Glu Lys His Ile Gln Cys Xaa Leu Lys His Val Leu Thr Xaa
515 520 525
His Xaa Val Cys Thr Gly Tyr Tyr Val Leu Gln Ile Ile Glu Gln Asp
530 535 540
Asp Gly Ser Glu Cys Tyr Val Phe Arg Lys Trp Gly Arg Val Gly Ser
545 550 555 560
Glu Lys Ile Gly Gly Gln Lys Leu Glu Glu Met Ser Lys Thr Glu Ala
565 570 575
Ile Lys Glu Phe Lys Arg Leu Phe Leu Glu Lys Thr Gly Asn Ser Trp
580 585 590
Glu Ala Trp Glu Cys Lys Thr Asn Phe Arg Lys Gln Pro Gly Arg Phe
595 600 605
Tyr Pro Leu Asp Val Asp Tyr Gly Val Lys Lys Ala Pro Lys Arg Lys
610 615 620
Asp Ile Ser Glu Met Lys Ser Ser Leu Ala Pro Gln Leu Leu Glu Leu
625 630 635 640
Met Lys Met Leu Phe Asn Val Glu Thr Tyr Arg Ala Ala Met Met Glu
645 650 655
Phe Glu Xaa Asn Met Ser Glu Met Pro Leu Gly Lys Leu Ser Xaa Xaa
660 665 670
Asn Ile Glu Xaa Gly Phe Glu Ala Leu Thr Xaa Xaa Xaa Xaa Leu Phe
675 680 685
Glu Gly His Arg Xaa Ser Ser Thr Gly Leu Xaa Glu Lys Ala Xaa Leu
690 695 700
Leu Xaa Xaa Xaa Xaa Xaa Phe Ser Leu Leu Ser Leu Leu Phe Ile Leu
705 710 715 720
Ile Leu Tyr Gly Met Arg Met Ile Ser Tyr Ser Lys Ala Lys Met Leu
725 730 735
Glu Ala Leu Gln Asp Ile Glu Ile Ala Ser Lys Ile Val Gly Phe Asp
740 745 750
Ser Asp Ser Asp Glu Ser Leu Asp Asp Lys Tyr Met Lys Leu His Cys
755 760 765
Asp Ile Thr Pro Leu Ala His Asp Ser Glu Asp Tyr Lys Leu Ile Glu
770 775 780
Gln Tyr Leu Leu Asn Thr His Ala Pro Thr His Lys Asp Trp Ser Leu
785 790 795 800
Glu Leu Glu Glu Val Phe Ser Leu Asp Arg Asp Gly Glu Leu Asn Lys
805 810 815
Tyr Ser Arg Tyr Lys Asn Asn Leu His Asn Lys Met Leu Leu Trp His
820 825 830
Gly Ser Arg Leu Thr Asn Phe Val Gly Ile Leu Ser Gln Gly Leu Arg
835 840 845
Ile Ala Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly
850 855 860

See
item 10
on Enw
Summary
Sheet

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/236,995A

DATE: 11/01/2000
TIME: 13:18:35

Input Set : A:\Polyadpl.app
Output Set : N:\CRF3\11012000\I236995A.raw

L:161 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:165 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:169 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:172 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:173 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:205 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:212 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:213 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID# 1
L:355 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:355 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:355 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:355 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:355 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID# 2
L:357 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:357 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:357 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:357 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
M:340 Repeated in SeqNo=2
L:359 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:359 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:359 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:359 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:361 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:361 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:361 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:361 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:377 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:377 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:377 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:377 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:379 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:379 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:379 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:379 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:381 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:381 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:381 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:381 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2
L:383 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID# 2
L:383 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID# 2
L:383 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID# 2
L:383 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID# 2